AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1-20 (canceled)

21.(new) A method for the study of inter-molecular interactions under physiological or near-physiological conditions, characterized in that
- the molecules of interest, being the same or different, are inserted as functional entities (FE) in a biomolecular complex comprising at least two functional elements (FE_1, FE_2) each attached to a target molecule or area (T) through binding elements (BE), wherein each FE is attached to a specific BE, said BE being a nucleotide sequence and the target molecule or area comprising the corresponding target sequence, and the target molecules or areas being separated from each other by a first linker or spacer (L) and an optional second linker (l), said linkers being nucleic acid polymers having a pre-determined physical property; and
- the orientation and distance between the molecules being varied by varying at least one of the first and second linker (L, l).

22.(new) The method according to claim 21, wherein receptors are screened with respect to their involvement in the internalisation of substances in a cell.

23.(new) The method according to claim 22, wherein the cells are chosen among eukaryotic and prokaryotic cells, and the

functional elements substituted by ligands presumed to interact with said receptors.

24.(new) Drug candidates identified using the method according to claim 21.

25.(new) Method for the production of a biomolecular complex comprising at least two functional elements (FE_1, FE_2) each attached to a target molecule or area (T) through binding elements (BE), wherein each FE is attached to a specific BE, said BE being a nucleotide sequence and the target molecule or area comprising the corresponding target sequence, and the target molecules or areas being separated from each other by a first linker or spacer (L) and an optional second linker (l), said linkers being nucleic acid polymer s having a pre-determined physical property; said method comprising the steps of

a) forming a stock solution of a first functional entity,

b) forming a stock solution of a second functional entity,

c) forming separate stock solutions of at least two binding entities,

d) forming separate stock solutions of nucleic acid molecules as linker molecules, each solution containing a linker having a distinct physical property,

e) reacting said first functional entity with at least one binding entity,

f) reacting said second functional entity with at least one binding entity, other than the binding entity in e)

g) repeating steps e) and f) for each functional entity,

h) reacting each linker molecule with at least two target molecules / target areas, capable of specific binding to the binding entities of e) and f)

i) reacting each combination of functional entity and binding entity with each linker, and

j) repeating step h) in order to form a library of combinations of functional entities and linkers.

26.(new) Method for the production of a biomolecular complex comprising at least two functional elements (FE_1, FE_2) each attached to a target molecule or area (T) through binding elements (BE), wherein each FE is attached to a specific BE, said BE being a nucleotide sequence and the target molecule or area comprising the corresponding target sequence, and the target molecules or areas being separated from each other by a first linker or spacer (L) and an optional second linker (l), said linkers being nucleic acid polymer s having a pre-determined physical property; said method comprising the steps of

i) synthesis of a molecular combination of a first functional entity and a first binding entity,

ii) synthesis of a molecular combination of said first functional entity and a second binding entity,

iii) synthesis of a molecular combination of a second functional entity and said first binding entity,

iv) synthesis of a molecular combination of a second functional entity and said second binding entity,

optionally repeating steps i) - iv) for further functional entities and binding entities and forming stock solutions thereof,

v) synthesis of a nucleic acid molecule as a linker connecting a first and second target area, and

vi) self-assembly of the molecular combinations of any one of step i) - iv) to the linker of step v) in the desired configuration by addition of these to said linker in solution.

27.(new) Method according to claim 25, wherein the linker molecule comprises a marker or label chosen among a reporter gene, a radioactive label, and a fluorescent label.

28.(new) Method according to claim 25, wherein the binding entities are PNA sequences.

29.(new) A combinatorial library produced by the method according to claim 25.

30.(new) A combinatorial library according to claim 29, wherein the functional entities are chosen among a natural or synthetic peptide, a lipid, a glycoprotein, a receptor ligand, and a fraction of any of the preceding.

31.(new) Drug delivery vectors produced using the method according to claim 25.

32.(new) Drug delivery vectors identified using a combinatorial library according to claim 29.

33.(new) Drug candidates identified using a combinatorial library according to claim 29.